



## SEQUENCE LISTING

<110> MORGAN, BRYAN P.  
RUSHMERE, NEIL K.  
HINCHLIFFE, STEWART J.  
VAN DEN BERG, CARMEN W.

<120> MODIFIED BIOLOGICAL MATERIAL

<130> WN/KH/JJ/WCM

<140> 09/673,032

<141> 2000-12-06

<150> PCT/GB99/01085

<151> 1999-04-08

<150> GB 9807520.3

<151> 1998-04-09

<160> 24

<170> PatentIn Ver. 2.1

<210> 1

<211> 123

<212> PRT

<213> Porcus sp.

<400> 1

Met Gly Ser Lys Gly Gly Phe Ile Leu Leu Trp Leu Leu Ser Ile Leu  
1 5 10 15

Ala Val Leu Cys His Leu Gly His Ser Leu Gln Cys Tyr Asn Cys Ile  
20 25 30

Asn Pro Ala Gly Ser Cys Thr Thr Ala Met Asn Cys Ser His Asn Gln  
35 40 45

Asp Ala Cys Ile Phe Val Glu Ala Val Pro Pro Lys Thr Tyr Tyr Gln  
50 55 60

Cys Trp Arg Phe Asp Glu Cys Asn Phe Asp Phe Ile Ser Arg Asn Leu  
65 70 75 80

Ala Glu Lys Lys Leu Lys Tyr Asn Cys Cys Arg Lys Asp Leu Cys Asn  
85 90 95

Lys Ser Asp Ala Thr Ile Ser Ser Gly Lys Thr Ala Leu Leu Val Ile  
100 105 110

Leu Leu Leu Val Ala Thr Trp His Phe Cys Leu  
115 120

<210> 2

<211> 773

<212> DNA

<213> Porcus sp.

<220>

<221> CDS

<222> (90) .. (458)

<400> 2

```

gaaaagacgc gcaggccggg ccgctctccc gacggggagt agcgctgcag ccggacgcag 60

ggtgcagtta gaatccatag acggtcacg atg gga agc aaa gga ggg ttc att 113
                               Met Gly Ser Lys Gly Gly Phe Ile
                               1           5

ttg ctc tgg ctc ctg tcc atc ctg gct gtt ctc tgc cac tta ggt cac 161
Leu Leu Trp Leu Leu Ser Ile Leu Ala Val Leu Cys His Leu Gly His
   10                   15                   20

agc ctg cag tgc tat aac tgt atc aac cca gct ggt agc tgc act acg 209
Ser Leu Gln Cys Tyr Asn Cys Ile Asn Pro Ala Gly Ser Cys Thr Thr
   25                   30                   35                   40

gcc atg aat tgt tca cat aat cag gat gcc tgt atc ttc gtt gaa gcc 257
Ala Met Asn Cys Ser His Asn Gln Asp Ala Cys Ile Phe Val Glu Ala
                   45                   50                   55

gtg cca ccc aaa act tac tac cag tgt tgg agg ttc gat gaa tgc aat 305
Val Pro Pro Lys Thr Tyr Tyr Gln Cys Trp Arg Phe Asp Glu Cys Asn
                   60                   65                   70

ttc gat ttc att tcg aga aac cta gcg gag aag aag ctg aag tac aac 353
Phe Asp Phe Ile Ser Arg Asn Leu Ala Glu Lys Lys Leu Lys Tyr Asn
   75                   80                   85

tgc tgc cgg aag gac ctg tgt aac aag agt gat gcc acg att tca tca 401
Cys Cys Arg Lys Asp Leu Cys Asn Lys Ser Asp Ala Thr Ile Ser Ser
   90                   95                   100

ggg aaa acc gct ctg ctg gtg atc ctg ctg ctg gta gca acc tgg cac 449
Gly Lys Thr Ala Leu Leu Val Ile Leu Leu Leu Val Ala Thr Trp His
  105                   110                   115                   120

ttt tgt ctc taactgtaca ccaggagagt ttctcctcaa ctctcctctgt 498
Phe Cys Leu

ctctctgttc ctatttccca tgctgcggtg ttccaaaggc tgtgtatgct ccagcttctt 558

cctggttgga aggactaaac ctagcttgag cactttggat tagagagaga aactttgagc 618

gactttgaag accaggcctg ttggcagaga agacctgtca gaggggaaac gttttaagag 678

tgaagcacag gtgatttgag cgaggcctat gcgtcttctt ctgctcttgg caggaccagc 738

tttgcggtaa ccattcgata gattccacaa tcctt 773

```

<210> 3

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 3

tgytayaayt gyathaa

17

<210> 4

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 4

agrtcyyt krcarca

17

<210> 5

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 5

ccagtgagca gagtgacgag gactcgagct caagct

36

<210> 6

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 6

ccagtgagca gagtgacg

18

<210> 7

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 7

gaggactcga gctcaagc

18

<210> 8  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 8  
 tgactacgg ccatgaattg 20

<210> 9  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 9  
 tcgtgaagc cgtgccaccc 20

<210> 10  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 10  
 aggtccttct tgcagcagtg 20

<210> 11  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 11  
 cttctccgct aggtttctcg 20

<210> 12  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 12  
 gcattcatcg aacctccaac 20

<210> 13  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 13  
 gggtctagag tagcgctgca gccggac

27

<210> 14  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 14  
 ggtggatcct tctctgcaa caggcct

27

<210> 15  
 <211> 1637  
 <212> DNA  
 <213> Porcus sp.

<220>  
 <221> modified\_base  
 <222> (17)  
 <223> a, t, c, g, other or unknown

<220>  
 <221> modified\_base  
 <222> (1323)  
 <223> a, t, c, g, other or unknown

<220>  
 <221> modified\_base  
 <222> (1330)  
 <223> a, t, c, g, other or unknown

<220>  
 <221> modified\_base  
 <222> (1357)  
 <223> a, t, c, g, other or unknown

<220>  
 <221> modified\_base  
 <222> (1378)  
 <223> a, t, c, g, other or unknown

<220>  
 <221> modified\_base

<222> (1403)  
<223> a, t, c, g, other or unknown

<220>  
<221> modified\_base  
<222> (1424)  
<223> a, t, c, g, other or unknown

<220>  
<221> modified\_base  
<222> (1437)  
<223> a, t, c, g, other or unknown

<220>  
<221> modified\_base  
<222> (1445)  
<223> a, t, c, g, other or unknown

<220>  
<221> modified\_base  
<222> (1513)  
<223> a, t, c, g, other or unknown

<220>  
<221> modified\_base  
<222> (1520)  
<223> a, t, c, g, other or unknown

<220>  
<221> modified\_base  
<222> (1527)  
<223> a, t, c, g, other or unknown

<220>  
<221> modified\_base  
<222> (1535)  
<223> a, t, c, g, other or unknown

<220>  
<221> modified\_base  
<222> (1544)  
<223> a, t, c, g, other or unknown

<220>  
<221> modified\_base  
<222> (1563)  
<223> a, t, c, g, other or unknown

<220>  
<221> modified\_base  
<222> (1588)  
<223> a, t, c, g, other or unknown

<220>  
<221> modified\_base  
<222> (1609)..(1611)  
<223> a, t, c, g, other or unknown

<220>  
 <221> modified\_base  
 <222> (1625)  
 <223> a, t, c, g, other or unknown

<400> 15  
 ccaccgcggt ggccggcncgc tctagaacta gtggatcccc cgggctgcag gaattcggca 60  
 cgagatttcg tcttaatcgc ggaggtcgca gagtccggga gccgctcggg gtccccgttc 120  
 ccgcgcgcca tgagtcacct gccgcggagc gccccgcgg tgaggcgcct aatgggcgga 180  
 cagacgccgc cggcgtgct gctgctgctg ctgctgctgt gtatcccggc tgcgcagggt 240  
 gactgcagcc ttccaccga tgtacctaat gcccaccag atttgcgagg tcttgcaagt 300  
 tttcctgaac aaaccacaat aacatacaaa tgtaacaaag gctttgtcaa agttcctggc 360  
 atggcagact cagtgtctctg tcttaatgat aaatggtcag aagttgcaga attttgtaat 420  
 cgtagctgtg atgttccaac caggctacat tttgcatctc ttaaaaagtc ttacagcaaa 480  
 cagaattatt tcccagaggg tttcaccgtg gaatatgagt gccgtaaggg ctataaaaagg 540  
 gatcttactc tatcagaaaa actaacttgc cttcagaatt ttacgtggtc caaacctgat 600  
 gaattttgca aaaaaaaaca atgtccgact cctggagaac taaaaaatgg tcatgtcaat 660  
 ataacaactg acttggtatt tggcgcaccc atctttttct catgtaacgc aggggtacaga 720  
 ctagttgggt caacttctag ttactgtttt gccatagcaa atgatgttga gtggagtgat 780  
 ccattgccag attgccaaaga aattttctcca actgtcaaag ccataccagc tgttgagaaa 840  
 cccatcacag taaattttcc agcaacaaag tatccagcta ttcccagggc cacaacgagt 900  
 tttcattcaa gtacatctaa aaatcgagga aacccttctt caggcatgag aatcatgtcg 960  
 tctggtacca tgctacttat tgcaggaggt gttgctgtta ttataataat tgttgcccta 1020  
 attctagcca aaggtttctg gcactatgga aaatcaggct cttaccacac tcatgagAAC 1080  
 aacaaagccg ttaatgttgc attttataat ttacctgcga ctggcgatgc cgcagatgta 1140  
 agacctggta attaacaaaa ggacgtgcac gtgtaacact gacagttttg cttatggtgc 1200  
 tagtaaccat tggctagctg acttagccaa agaagagtta agaagaaagt gcacacaagt 1260  
 acacagaata ttttcagttt cttaaaactt tcaggtggga gtggacatag tttgtggtag 1320  
 tgnctctcgn tttgcatggg ttcatgtggc ctaaggnaca taggaatgca cagaaccnaa 1380  
 gagaaacaaa tctatcctga aantacatcc tcaacacttc taanactctt ggaaatngaa 1440  
 caagntcata agattgggag caattacttt cccaaaaggg tgagaaaaat ggagaaattt 1500  
 ggtcatgggt agnaattttt gaaaaangaa acccnaaagg gganttttcc ccccaaaagg 1560  
 ggnaagggtta tttttattta attaaggnaa aaaaaaaaaa aaaaaccnng ngggggggcc 1620  
 cggncccat tttccct 1637

<210> 16  
 <211> 978  
 <212> DNA  
 <213> Porcus sp.

<400> 16  
 cagcagccgc cgcgcgtgct gctgctgctg ctgctgctgt gtatcccggc tgcgcagggt 60  
 gactgcagcc ttccaccga tgtacctaat gcccaccag atttgcgagg tcttgcaagt 120  
 tttcctgaac aaaccacaat aacatacaaa tgtaacaaag gctttgtcaa agttcctggc 180  
 atggcagact cagtgtctctg tcttaatgat aaatggtcag aagttgcaga attttgtaat 240  
 cgtagctgtg atgttccaac caggctacat tttgcatctc ttaaaaagtc ttacagcaaa 300  
 cagaattatt tcccagaggg tttcaccgtg gaatatgagt gccgtaaggg ctataaaaagg 360  
 gatcttactc tatcagaaaa actaacttgc cttcagaatt ttacgtggtc caaacctgat 420  
 gaattttgca aaaaaaaaca atgtccgact cctggagaac taaaaaatgg tcatgtcaat 480  
 ataacaactg acttggtatt tggcgcaccc atctttttct catgtaacgc aggggtacaga 540  
 ctagttgggt caacttctag ttactgtttt gccatagcaa atgatgttga gtggagtgat 600  
 ccattgccag aatgccaaaga aattttctcca actgtcaaag ccataccagc tgttgagaaa 660  
 cccatcacag taaattttcc aggtacacaa gccctatcat ctctcagaa accctocaca 720  
 gcaaatactc tagctacaga gttactacca actcctcagg aaccaccac agtaaatgtt 780  
 ccagatagta aagccatatc atctcctcag aaaccctcca cagtaaatac tccagctaca 840

```

gacttactac caactcctca ggaacccacc acagtaaatg ttccagatag taaagccata 900
tcattctctc agaaaccctc cacagtaaat actccagctc agacttacta ccaactcctc 960
aggaaccac cacagtaa                                     978

```

```

<210> 17
<211> 327
<212> PRT
<213> Porcus sp.

```

```

<220>
<221> MOD_RES
<222> (322)
<223> Any amino acid

```

```

<400> 17
Met Gly Gly Gln Thr Pro Pro Pro Leu Leu Leu Leu Leu Leu Leu
  1              5              10              15

Cys Ile Pro Ala Ala Gln Gly Asp Cys Ser Leu Pro Pro Asp Val Pro
          20              25              30

Asn Ala Gln Pro Asp Leu Arg Gly Leu Ala Ser Phe Pro Glu Gln Thr
      35              40              45

Thr Ile Thr Tyr Lys Cys Asn Lys Gly Phe Val Lys Val Pro Gly Met
      50              55              60

Ala Asp Ser Val Leu Cys Leu Asn Asp Lys Trp Ser Glu Val Ala Glu
      65              70              75              80

Phe Cys Asn Arg Ser Cys Asp Val Pro Thr Arg Leu His Phe Ala Ser
          85              90              95

Leu Lys Lys Ser Tyr Ser Lys Gln Asn Tyr Phe Pro Glu Gly Phe Thr
      100              105              110

Val Glu Tyr Glu Cys Arg Lys Gly Tyr Lys Arg Asp Leu Thr Leu Ser
      115              120              125

Glu Lys Leu Thr Cys Leu Gln Asn Phe Thr Trp Ser Lys Pro Asp Glu
      130              135              140

Phe Cys Lys Lys Lys Gln Cys Pro Thr Pro Gly Glu Leu Lys Asn Gly
      145              150              155              160

His Val Asn Ile Thr Thr Asp Leu Leu Phe Gly Ala Ser Ile Phe Phe
          165              170              175

Ser Cys Asn Ala Gly Tyr Arg Leu Val Gly Ala Thr Ser Ser Tyr Cys
          180              185              190

Phe Ala Ile Ala Asn Asp Val Glu Trp Ser Asp Pro Leu Pro Asp Cys
      195              200              205

Gln Glu Ile Ser Pro Thr Val Lys Ala Ile Pro Ala Val Glu Lys Pro
      210              215              220

```



Ile Thr Val Asn Phe Pro Ala Thr Lys Tyr Pro Ala Ile Pro Arg Ala  
 225 230 235 240

Thr Thr Ser Phe His Ser Ser Thr Ser Lys Asn Arg Gly Asn Pro Ser  
 245 250 255

Ser Gly Met Arg Ile Met Ser Ser Gly Thr Met Leu Leu Ile Ala Gly  
 260 265 270

Gly Val Ala Val Ile Ile Ile Ile Val Ala Leu Ile Leu Ala Lys Gly  
 275 280 285

Phe Trp His Tyr Gly Lys Ser Gly Ser Tyr His Thr His Glu Asn Asn  
 290 295 300

Lys Ala Val Asn Val Ala Phe Tyr Asn Leu Pro Ala Thr Gly Asp Ala  
 305 310 315 320

Ala Xaa Val Arg Pro Gly Asn  
 325

<210> 18  
 <211> 325  
 <212> PRT  
 <213> Porcus sp.

<400> 18  
 His Glu Pro Pro Pro Leu Leu Leu Leu Leu Leu Leu Cys Ile Pro  
 1 5 10 15

Ala Ala Gln Gly Asp Cys Ser Leu Pro Pro Asp Val Pro Asn Ala Gln  
 20 25 30

Pro Asp Leu Arg Gly Leu Ala Ser Phe Pro Glu Gln Thr Thr Ile Thr  
 35 40 45

Tyr Lys Cys Asn Lys Gly Phe Val Lys Val Pro Gly Met Ala Asp Ser  
 50 55 60

Val Leu Cys Leu Asn Asp Lys Trp Ser Glu Val Ala Glu Phe Cys Asn  
 65 70 75 80

Arg Ser Cys Asp Val Pro Thr Arg Leu His Phe Ala Ser Leu Lys Lys  
 85 90 95

Ser Tyr Ser Lys Gln Asn Tyr Phe Pro Glu Gly Phe Thr Val Glu Tyr  
 100 105 110

Glu Cys Arg Lys Gly Tyr Lys Arg Asp Leu Thr Leu Ser Glu Lys Leu  
 115 120 125

Thr Cys Leu Gln Asn Phe Thr Trp Ser Lys Pro Asp Glu Phe Cys Lys  
 130 135 140

Lys Lys Gln Cys Pro Thr Pro Gly Glu Leu Lys Asn Gly His Val Asn  
 145 150 155 160

Ile Thr Thr Asp Leu Leu Phe Gly Ala Ser Ile Phe Phe Ser Cys Asn  
 165 170 175

Ala Gly Tyr Arg Leu Val Gly Ala Thr Ser Ser Tyr Cys Phe Ala Ile  
 180 185 190

Ala Asn Asp Val Glu Trp Ser Asp Pro Leu Pro Glu Cys Gln Glu Ile  
 195 200 205

Ser Pro Thr Val Lys Ala Ile Pro Ala Val Glu Lys Pro Ile Thr Val  
 210 215 220

Asn Phe Pro Gly Thr Lys Ala Leu Ser Ser Pro Gln Lys Pro Ser Thr  
 225 230 235 240

Ala Asn Thr Leu Ala Thr Glu Leu Leu Pro Thr Pro Gln Glu Pro Thr  
 245 250 255

Thr Val Asn Val Pro Asp Ser Lys Ala Ile Ser Ser Pro Gln Lys Pro  
 260 265 270

Ser Thr Val Asn Thr Pro Ala Thr Asp Leu Leu Pro Thr Pro Gln Glu  
 275 280 285

Pro Thr Thr Val Asn Val Pro Asp Ser Lys Ala Ile Ser Ser Ser Gln  
 290 295 300

Lys Pro Ser Thr Val Asn Thr Pro Ala Gln Thr Tyr Tyr Gln Leu Leu  
 305 310 315 320

Arg Asn Pro Pro Gln  
 325

<210> 19

<211> 376

<212> PRT

<213> Homo sapiens

<400> 19

Pro Ser Val Pro Ala Ala Leu Pro Leu Leu Gly Glu Leu Pro Arg Leu  
 1 5 10 15

Leu Leu Leu Val Leu Leu Cys Leu Pro Ala Val Trp Gly Asp Cys Gly  
 20 25 30

Leu Pro Pro Asp Val Pro Asn Ala Gln Pro Ala Leu Glu Gly Arg Thr  
 35 40 45

Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys Cys Glu Glu Ser Phe  
 50 55 60

Val Lys Ile Pro Gly Glu Lys Asp Ser Val Thr Cys Leu Lys Gly Met  
 65 70 75 80

Gln Trp Ser Asp Ile Glu Glu Phe Cys Asn Arg Ser Cys Glu Val Pro  
 85 90 95

Thr Arg Leu Asn Ser Ala Ser Leu Lys Gln Pro Tyr Ile Thr Gln Asn  
 100 105 110  
 Tyr Phe Pro Val Gly Thr Val Val Glu Tyr Glu Cys Arg Pro Gly Tyr  
 115 120 125  
 Arg Arg Glu Pro Ser Leu Ser Pro Lys Leu Thr Cys Leu Gln Asn Leu  
 130 135 140  
 Lys Trp Ser Thr Ala Val Glu Phe Cys Lys Lys Lys Ser Cys Pro Asn  
 145 150 155 160  
 Pro Gly Glu Ile Arg Asn Gly Gln Ile Asp Val Pro Gly Gly Ile Leu  
 165 170 175  
 Phe Gly Ala Thr Ile Ser Phe Ser Cys Asn Thr Gly Tyr Lys Leu Phe  
 180 185 190  
 Gly Ser Thr Ser Ser Phe Cys Leu Ile Ser Gly Ser Ser Val Gln Trp  
 195 200 205  
 Ser Asp Pro Leu Pro Glu Cys Arg Glu Ile Tyr Cys Pro Ala Pro Pro  
 210 215 220  
 Gln Ile Asp Asn Gly Ile Ile Gln Gly Glu Arg Asp His Tyr Gly Tyr  
 225 230 235 240  
 Arg Gln Ser Val Thr Tyr Ala Cys Asn Lys Gly Phe Thr Met Ile Gly  
 245 250 255  
 Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp Glu Gly Glu Trp Ser  
 260 265 270  
 Gly Pro Pro Pro Glu Cys Arg Gly Lys Ser Leu Thr Ser Lys Val Pro  
 275 280 285  
 Pro Thr Val Gln Lys Pro Thr Thr Val Asn Val Pro Thr Thr Glu Val  
 290 295 300  
 Ser Pro Thr Ser Gln Lys Thr Thr Thr Lys Thr Thr Thr Pro Asn Ala  
 305 310 315 320  
 Gln Ala Thr Arg Ser Thr Pro Val Ser Arg Thr Thr Lys His Phe His  
 325 330 335  
 Glu Thr Thr Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg  
 340 345 350  
 Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr  
 355 360 365  
 Leu Val Thr Met Gly Leu Leu Thr  
 370 375

<210> 20  
 <211> 128  
 <212> PRT

<213> Homo sapiens

<400> 20

```

Met Gly Ile Gln Gly Gly Ser Val Leu Phe Gly Leu Leu Leu Val Leu
 1           5           10           15

Ala Val Phe Cys His Ser Gly His Ser Leu Gln Cys Tyr Asn Cys Pro
          20           25           30

Asn Pro Thr Ala Asp Cys Lys Thr Ala Val Asn Cys Ser Ser Asp Phe
          35           40           45

Asp Ala Cys Leu Ile Thr Lys Ala Gly Leu Gln Val Tyr Asn Lys Cys
          50           55           60

Trp Lys Phe Glu His Cys Asn Phe Asn Asp Val Thr Thr Arg Leu Arg
 65           70           75           80

Glu Asn Glu Leu Thr Tyr Tyr Cys Cys Lys Lys Asp Leu Cys Asn Phe
          85           90           95

Asn Glu Gln Leu Glu Asn Gly Gly Thr Ser Leu Ser Glu Lys Thr Val
          100          105          110

Leu Leu Leu Val Thr Pro Phe Leu Ala Ala Ala Trp Ser Leu His Pro
          115          120          125

```

<210> 21

<211> 126

<212> PRT

<213> Rattus sp.

<400> 21

```

Met Arg Ala Arg Arg Gly Phe Ile Leu Leu Leu Leu Leu Ala Val Leu
 1           5           10           15

Cys Ser Thr Gly Val Ser Leu Arg Cys Tyr Asn Cys Leu Asp Pro Val
          20           25           30

Ser Ser Cys Lys Thr Asn Ser Thr Cys Ser Pro Asn Leu Asp Ala Cys
          35           40           45

Leu Val Ala Val Ser Gly Lys Gln Val Tyr Gln Gln Cys Trp Arg Phe
          50           55           60

Ser Asp Cys Asn Ala Lys Phe Ile Leu Ser Arg Leu Glu Ile Ala Asn
          65           70           75           80

Val Gln Tyr Arg Cys Cys Gln Ala Asp Leu Cys Asn Lys Ser Phe Glu
          85           90           95

Asp Lys Pro Asn Asn Gly Ala Ile Ser Leu Leu Gly Lys Thr Ala Leu
          100          105          110

Leu Val Thr Ser Val Leu Ala Ala Ile Leu Lys Pro Cys Phe
          115          120          125

```

<210> 22  
 <211> 123  
 <212> PRT  
 <213> Murine sp.

<400> 22  
 Met Arg Ala Gln Arg Gly Leu Ile Leu Leu Leu Leu Leu Ala Val  
     1                    5                    10                    15  
 Phe Cys Ser Thr Ala Val Ser Leu Thr Cys Tyr His Cys Phe Gln Pro  
                     20                    25                    30  
 Val Val Ser Ser Cys Asn Met Asn Ser Thr Cys Ser Pro Asp Gln Asp  
                     35                    40                    45  
 Ser Cys Leu Tyr Ala Val Ala Gly Met Gln Val Tyr Gln Arg Cys Trp  
                     50                    55                    60  
 Lys Gln Ser Asp Cys His Gly Glu Ile Ile Met Asp Gln Leu Glu Glu  
     65                    70                    75                    80  
 Thr Lys Leu Lys Phe Arg Cys Cys Gln Phe Asn Leu Cys Asn Lys Ser  
                     85                    90                    95  
 Asp Gly Ser Leu Gly Lys Thr Pro Leu Leu Gly Thr Ser Val Leu Val  
                     100                    105                    110  
 Ala Ile Leu Asn Leu Cys Phe Leu Ser His Leu  
                     115                    120

<210> 23  
 <211> 6  
 <212> PRT  
 <213> Homo sapiens

<400> 23  
 Cys Cys Lys Lys Asp Leu  
     1                    5

<210> 24  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Illustrative  
       peptide

<220>  
 <221> MOD\_RES  
 <222> (7)  
 <223> Any amino acid

<220>  
 <221> MOD\_RES

<222> (10)

<223> Any amino acid

<400> 24

Asp Cys Gly Leu Pro Pro Xaa Val Pro Xaa Ala Gln Pro Ala  
1 5 10